

CLAIMS

What is claimed is:

5 1. A nucleic acid primer comprising an oligonucleotide that selectively hybridizes to a highly conserved region of a nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain.

10 2. The primer of Claim 1 wherein the oligonucleotide hybridizes to a region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

15 3. The primer of Claim 1 wherein the oligonucleotide hybridizes to a region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting of 4550 to 4625; 4626 to 4753; 4754 to 4984; 4985 to 5126; 4596 to 4625; 4724 to 4753; 4956 to 4984; and 5051 to 5080.

20 4. The primer of Claim 1 having a length of 18-40 nucleotides.

25 5. The primer of Claim 1 wherein the oligonucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and conservative substitutions thereof.

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6. A method of detecting HIV-1 groups M, N and O and SIVcpz in a biological sample comprising

5 combining the sample with a first primer under selective hybridization conditions for the selective hybridization of the first primer to HIV-1 nucleic acids in the sample, wherein the first primer comprises an oligonucleotide that selectively hybridizes to a highly conserved region of the nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain; and

10 detecting hybridization of the primer to HIV-1 nucleic acids,

wherein detection of hybridization of the primer to HIV-1 nucleic acids indicates the presence of HIV-1 in the sample.

15 7. The method of Claim 6 wherein the first primer hybridizes to a first region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

25 8. The method of Claim 6 wherein the first primer hybridizes to a first region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting 4550 to 4625; 4626 to 4753; 4754 to 4984; 4596 to 4625; 4724 to 4753; and 4956 to 4984; and 8265 to 8294.

30 9. The method of Claim 6 wherein the oligonucleotide has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and conservative substitutions thereof.

10. The method of Claim 6 further comprising the step of combining the sample with a second primer under selective hybridization conditions for the selective hybridization of the second primer to HIV-1 nucleic acids in the sample, wherein the second primer comprises an oligonucleotide that selectively hybridizes to a second highly conserved region of the nucleic acid molecule of HIV-1 between nucleotide positions 4550 and 5126 or 7746 and 8459 of the HXB2 strain, wherein the first and second primers are a first primer pair, and wherein the primer pair and the sample are incubated under nucleic acid amplification conditions to amplify HIV-1 nucleic acids in the sample.

15. The method of Claim 10 wherein the second primer hybridizes to a second region of the *env* gene of HIV-1 between nucleotide positions selected from the group consisting of 7746 to 7772; 7817 to 7844; 8220 to 8258; 8432 to 8459; 7789 to 7816; 8347 to 8374; 7850 to 7879; 8265 to 8294; and 8281 to 8310.

20. The method of Claim 10 wherein the second primer hybridizes to a second region of the *pol* gene of HIV-1 between nucleotide positions selected from the group consisting of 4550 to 4625; 4626 to 4753; 4754 to 4954; 4885 to 5126; 4596 to 4625; 4724 to 4753; 4956 to 4984; and 5051 to 5080.

25. The method of Claim 10 wherein the second primer has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and conservative substitutions thereof.

14. The method of Claim 10 wherein the first primer pair comprises a forward primer and a reverse primer, wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:1 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:2, or wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:6 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:7.

15. The method of Claim 10 further comprising a second primer pair, wherein the first and second primer pairs are nested.

16. The method of Claim 15 wherein the second primer pair comprises a forward primer and a reverse primer, wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:3 and the reverse primer comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:5, or wherein the forward primer comprises the nucleotide sequence of SEQ ID NO:8 and the reverse primer comprises the nucleotide sequence of SEQ ID NO:9.

17. A method for detecting HIV-1 group N or chimpanzee SIV in a biological sample comprising
combining the sample with a first primer under selective hybridization conditions for the selective hybridization of the first primer to HIV-1 or chimpanzee SIV nucleic acids in the sample, wherein the first primer comprises the nucleotide sequence of SEQ ID NO:5; SEQ ID NO:6, SEQ ID NO:7; SEQ ID NO:8, and SEQ ID NO:9 and
detecting hybridization of the primer to HIV-1 or chimpanzee SIV nucleic acids,
wherein detection of hybridization of the primer to HIV-1 or chimpanzee SIV nucleic acids indicates the presence of HIV-1 or chimpanzee SIV in the sample.

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18. The method of Claim 17 further comprising a second primer that hybridizes to a second highly conserved region of the nucleic acid molecule between nucleotide positions 4450 and 5126 or 7746 and 8459 of the HXB2 strain of HIV-1, wherein the first and second primers are a primer pair, and wherein the primer pair and the sample are incubated under nucleic acid amplification conditions to amplify HIV-1 nucleic acids in the sample.

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19. The method of Claim 18 wherein the second primer has a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and conservative substitutions thereof.

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